

1	GACGCGGCTGGCACTGGGTGGCGCCACACGCTGGCCACAACCTCCGGGCTCGCG	60
1	R G W H W V G A H T L G H N S R G F G V	20
61	TGGCCATAGTGGGCAACTACACCGCGGCGCTGCCACCGAGGCCGCTCTGCGCACGGTGC	120
21	A I V G N Y T A A L P T E A A L R T V R	40
121	GCGACACGCTCCGAGTTGTGCGGTGCGCGCCGGCCTCCTGCGGCCAGACTACGCGCTGC	180
41	D T L P S C A V R A G L L R P D Y A L L	60
181	TGGGCCACCGCCAGCTGGTGCACCGACTGCCCGGCGACGCGCTCTCGACCTGCTGC	240
61	G H R Q L V R T D C P G D A L F D L L R	80
241	GCACCTGGCCGCACCCACCGCGGTGAGTCTTCGCAGCCTGCACGACTACACGGCCGCCGCC	300
81	T W P H F T A V S L R S L H Y T A R R P	100
301	CCTCCGTCTACACAAGCTCCACGAGGCCCTGCCCTGCCTGTAACAGCTGTGCCCGCA	360
101	S V Y T S S T R P L P P A C N S C A R T	120
361	CAGCCTCAGCCAGGCCAACTTCCGGCGCACGTCTATTCAAGAACCTAGGCCAG	420
121	A S A R P P T S R R H V Y S G N L G P A	140
421	CCTTGCGGGTCACTCTGCGGGCAACATCCCTGATCCTGTGACTTCTGCCTATGCAGCCT	480
141	F A G H S A G N I P D P V F S A Y A A S	160
481	CAGCTCAGCCCCAGACCCAGCCAGCCTGTCCTTCCCCAGCTCCTAACCTCTACCTT	540
161	A Q P Q T Q P A C P F P S S	174
541	CCAGCCAAGGCATGGACCCGTACACCTGCCAACAGCCCCCTGCCCTACAAACCTCAGCC	600
601	TGGCCTTCATGACTTCTACCCAAAGTCACAACCTGTCAGGCTGCACCACCTCATCCTGG	660
661	CCCGCCGAACCTTGACCTCACCCCTGCCCTACCGAAGGCTCTGTCCACACAAACATG	720

721 AACCTAGGCTGTGACCTTCGCCTCACAAACCTCTGTCCAGTCCTTAATCCTGTGCA 780
781 ATTCTCTGTCCAGACAATCTCAACTCTGAGGTTGCTTGTCCCTGACTCCTTAACC 840
841 CCTGATGACAACACTTTATGCCAGCACAACTTGACCTGATGACCTCATCCCAGCCCTG 900
901 TCGCCATCACTAAAACAATTTAGAATCACACCTGGACAATCTCGTGCTACCTACACT 960
961 GCCACTCCATTCATTAAGCTATTGACTAGCACATCCATCTGGCCTATAGTTGGCTTG 1020
1021 TCCTCACTCTCACTTGGGCCACTGTCCCCTCCCTGATAAAGGGGATATCACCACCGA 1080
1081 TCCCACAGAAATACAAACTACCATCAGAGAATACTATAAACACCTCTATGCAAATAACT 1140
1041 AGAAAATCTAGAAGAAATGGATAAATTCTCAACACCCACTACCAAAAAAAA 1200

FIG. 1B

1	GCCGTATGTGAGGTAAGCAGCTTCTCCAACAGAACAGAGTCCTCTCCTCAAAGGCCAG	60
61	AGTGTCCAGGCCAACCAACTGACCAAGAATTACAACGTGCTGAAACTGGCCTCCGAGGTTC	120
121	TCTGCTGGTCTGTGCCCTGGAACTGGAGACCCACCATGAAGGCCTGGGTGCCCTCTGG	180
1	M K A W G A L W	8
181	ATCGTGTGGATTGCTGCTGTGGCCAGAGCCAGGGCAGCCTCCTGCCTCTGCTC	240
9	I V L G L L W P E P G A A S S L P L L	28
241	ATGGACTCCATCATCCAGGCCCTGCTGAACCTGAGCAAAAGGTACCAAGTGACTGAGGCC	300
29	M D S I I Q A L A E L E Q K V P V T E A	48
301	AGCATCACTGCCTCTGCATGGATTCTGTCAGCCAAGAACCTCCAGCACCCACAATTCCCTT	360
49	S I T A S A W I L S A K N S S T H N S L	68
361	CACCAGCGCTTGCTGCTGAAGGCACCAAGCCACAACACTACAGAGCCAGATCCTCACTCT	420
69	H Q R L L K A P S H N T T E P D P H S	88
421	CTCAGCCGGAGCTCAAGCACTGATTCTGAGGTGGCTAACACGATGTACAGAATGGG	480
89	L S P E L Q A L I S E V A Q H D V Q N G	108
481	CGGGAATATGGAGTGGTGCTGGCACCTGATGGCTCCACCGTAGCTGTGAAGCCTCTGCTG	540
109	R E Y G V V L A P D G S T V A V K P L L	128
541	TTTGGGCTAGAGGCCGGTCTACAGGCACACAGCGTGCTAACTTGCCTTCAGATTGTCTG	600
129	F G L E A G L Q A H S V A N L P S D C L	148
601	GCTATCCCCTGTGATACTGGAGACACCTGGCCAATATTAGAGCCACCTGGCCAGGACTC	660
149	A I P C D T G D T L A N I R A T W P G L	168
661	ATGGATGCTTCCAAATGCCTCTCCAGATGTTGGAGCCACTTACCAAACGACAAA	720
169	M D A F P N A S S S P D V G A T L P N D K	188

721	GCCAAGACTCCCACCACTGTGGACAGACTCCTGGCAATCACCTGGCTGGTACTTAGGT	780
189	A K T P T T V D R L L A I T L A G D L G	208
781	CTGACCTTCCTCCACAGGTCCCAGACTTGGAGTCCTCCAGGACTGGGAAC TGAGGGCTGC	840
209	L T F L H R S Q T W S P P G L G T E G C	228
841	TGGGACCAGCTTACTGCC C CAGGGTCTTCACACTGTTGGACCCCCAGGCATCCAGGCTC	900
229	W D Q L T A P R V F T L L D P Q A S R L	248
901	ACCATGGCTTCCTCAATGGTGCCTAGATGGAGCTCTCCTGGGAACCACTTGAGCAA	960
249	T M A F L N G A L D G A L L L G N H L S Q	268
961	ATCCCTAGGCC CACCCACCCCTCAGCCACCTGCTAAGAGAGTACTATGGAGCTGGGTG	1020
269	I P R P H P P L S H L L R E Y Y G A G V	288
1021	AATGGAGATCCGGTGTCCGAAGTAACCTCCGAAGGCAGAACGGTGCTGCTTGACTTCA	1080
289	N G D P V F R S N F R R Q N G A A L T S	308
1081	GCCCCTACCCTGGCCCAGCAGGTATGGGAGGCCCTGTCCCTGTTACAGAAACTGGAGCA	1140
309	A P T L A Q Q V W E A L V L L Q K L E P	328
1141	GAACACCTACAGTTGCAGAACATTAGCCAAGAGCAGCTGGCTCAGGTAGCCACCTGGCT	1200
329	E H L Q L Q N I S Q E Q L A Q V A T L A	348
1201	ACCAAGGAGTTCACTGAGGCTTCCTGGATGCCAGCCATTACCCCCGCTGCCGTGG	1260
349	T K E F T E A F L G C P A I H P R C R W	368
1261	GGAGCGGCTCCCTACCGAGGCCACCCAACACCACTCCGGCTGCCACTTGGATTCTTATAT	1320
369	G A A P Y R G H P T P L R L P L G F L Y	388
1321	GTGCATCACACATACGTGCCAGCGCCACCCCTGCACCACCTCCAGAGCTGCGCCGCGAT	1380
389	V H H T Y V P A P P C T T F Q S C A A D	408

1381	ATGCGCTCCATGCAGCGTTCCACCAGGATGTGCGCAAGTGGGATGACATCGGCTACAGT	1440
409	M R S M Q R F H Q D V R K W D D I G Y S	428
1441	TTCGTGGTAGGCTCCGACGGCTATCTGTACCAGGGCCGTGGCCTGGCACTGGTAGGTGCG	1500
429	F V V G S D G Y L Y Q G R G W H W V G A	448
1501	CACACACGCGGCTACAACCTCCCGCGGCTTCGGTGTGGCCTCGTGGCAACTACACTGGG	1560
449	H T R G Y N S R G F G V A F V G N Y T G	468
1561	TCACTGCCAACGAAGCTGCGCTGAACACGGTGCACGCGCTCCGAGCTGCGCAATT	1620
469	S L P N E A A L N T V R D A L P S C A I	488
1621	CGCGAAGGTCTCTGCGGCCAGACTACAAGCTGCTGGCCACCGCCAGCTAGTGCTCACC	1680
489	R E G L L R P D Y K L L G H R Q L V L T	508
1681	CACTGCCCGGAAACGGCTCTCAACTGCTGCCACCTGGCCTCACTCACAGAGGTT	1740
509	H C P G N A L F N L L R T W P H F T E V	528
1741	GAAAAGTAAGAACTCCTTGAGAGAGCCCTGAAGATCCAGGAGGTATTATCCCTGATGAT	1800
529	E N *	531
1801	CCTTGAGCAACCACAGACCTCCAATAAAGGGACCACTGAAAGGAAAAAAAAAAAAAA	1860
1861	AAAAAAAAAAAAAAA 1876	

FIG. 2C

10 20 30 40

1 hPGRP-L aa Seq.
 1 MKAWGALWIVLGLLWPEPGAASSLPLLMDSIIQALAELE mPGRP-L aa Seq.

50 60 70 80

1 hPGRP-L aa Seq.
 41 QKVPVTEASITASAWILSAKNSSTHNSLHQRLLLKAPSHN mPGRP-L aa Seq.

90 100 110 120

1 hPGRP-L aa Seq.
 81 TTEPDPHSLSPELQALISEVAQHDVQNGREYGVVLAPDGS mPGRP-L aa Seq.

130 140 150 160

1 hPGRP-L aa Seq.
 121 TVAVKPLLFGLEAGLQAHHSVANLPSDCLAIPCDTGDTLAN mPGRP-L aa Seq.

170 180 190 200

1 hPGRP-L aa Seq.
 161 IRATWPGLMDAFTPNAASSPDVGATLPNDKAKTPTTVDRLLA mPGRP-L aa Seq.

210 220 230 240

1 hPGRP-L aa Seq.
 201 ITLAGDLGLTFLHRSQTWSPPGLGTEGCWDQLTAPRVFTL mPGRP-L aa Seq.

250 260 270 280

1 hPGRP-L aa Seq.
 241 LDPOQASRLTMAFLNGALDGALLGNHLSQIPRPHPPPLSHLL mPGRP-L aa Seq.

290 300 310 320

1 hPGRP-L aa Seq.
 281 REYYGAGVNGDPVFRSNFRRQNGAALTSAPTLAQQVWEAL mPGRP-L aa Seq.

FIG. 3A

330 340 350 360

1 ----- hPGRP-L aa Seq.
 321 VLLQKLEPEHLQLQNI S Q E Q L A Q V A T L A T K E F T E A F L G C P mPGRP-L aa Seq.

370 380 390 400

1 ----- hPGRP-L aa Seq.
 361 A I H P R C R W G A A P Y R G H P T P L R L P L G F L Y V H H T Y V P A P P C T mPGRP-L aa Seq.

410 420 430 440

1 ----- hPGRP-L aa Seq.
 401 T F Q S C A A D M R S M Q R F H Q D V R K W D D I G Y S F V V G S D G Y L Y Q G mPGRP-L aa Seq.

450 460 470 480

1 R G W H W V G A H T L G H N S R G F G V A I V G N Y T A A L P T E A A L R T V R hPGRP-L aa Seq.
 441 R G W H W V G A H T R G Y N S R G F G V A F V G N Y T G S L P N E A A L N T V R mPGRP-L aa Seq.

490 500 510 520

41 D T L P S C A V R A G L L R P D Y A L L G H R Q L V R T D C P G D A L F D L L R hPGRP-L aa Seq.
 481 D A L P S C A I R E G L L R P D Y K L L G H R Q L V L T H C P G N A L F N L L R mPGRP-L aa Seq.

530 540 550 560

81 T W P H F T A V S L R S L H Y T A R R P S V Y T S S T R P L P P A C N S C A R T hPGRP-L aa Seq.
 521 T W P H F T E V E ----- mPGRP-L aa Seq.

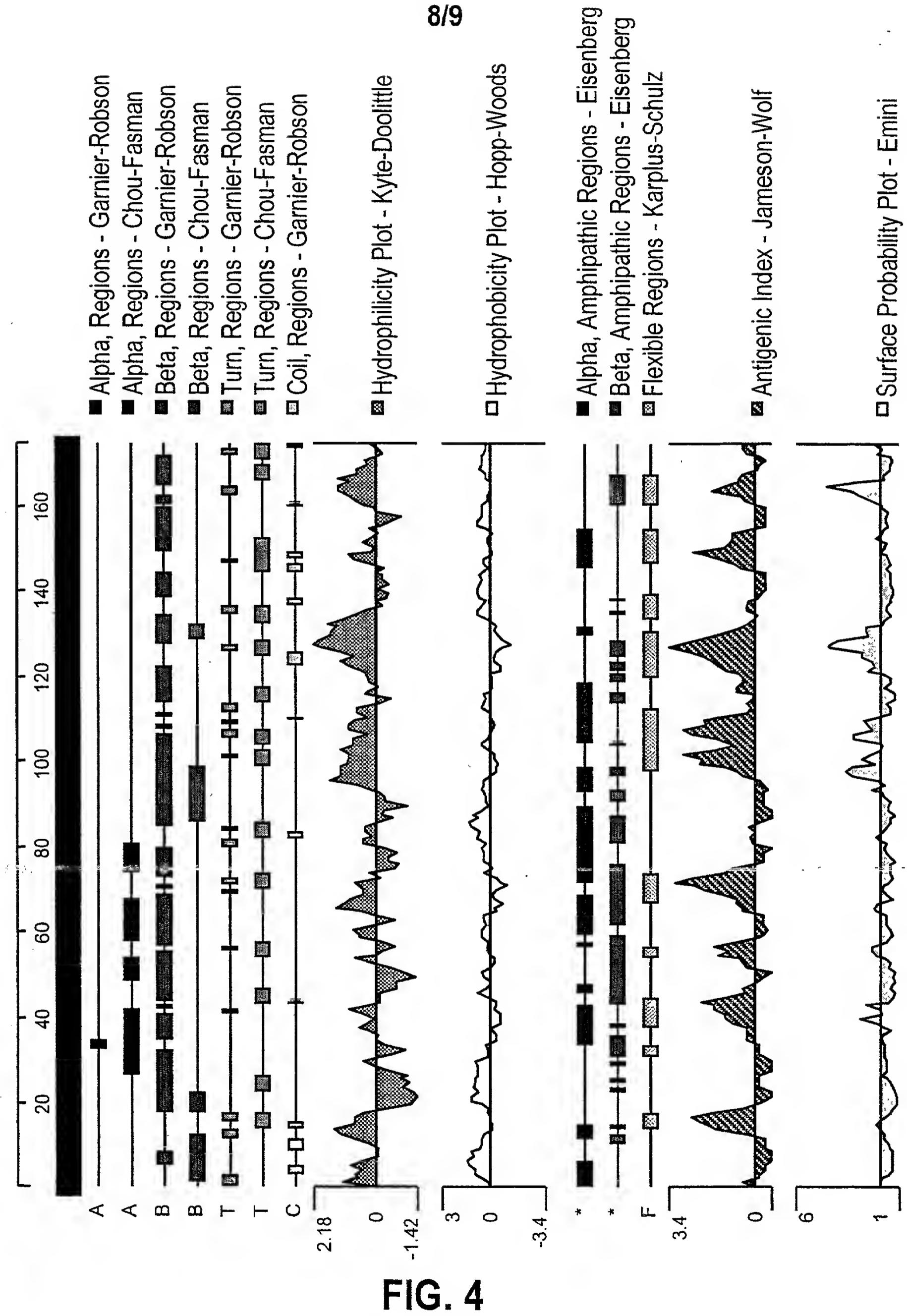
570 580 590 600

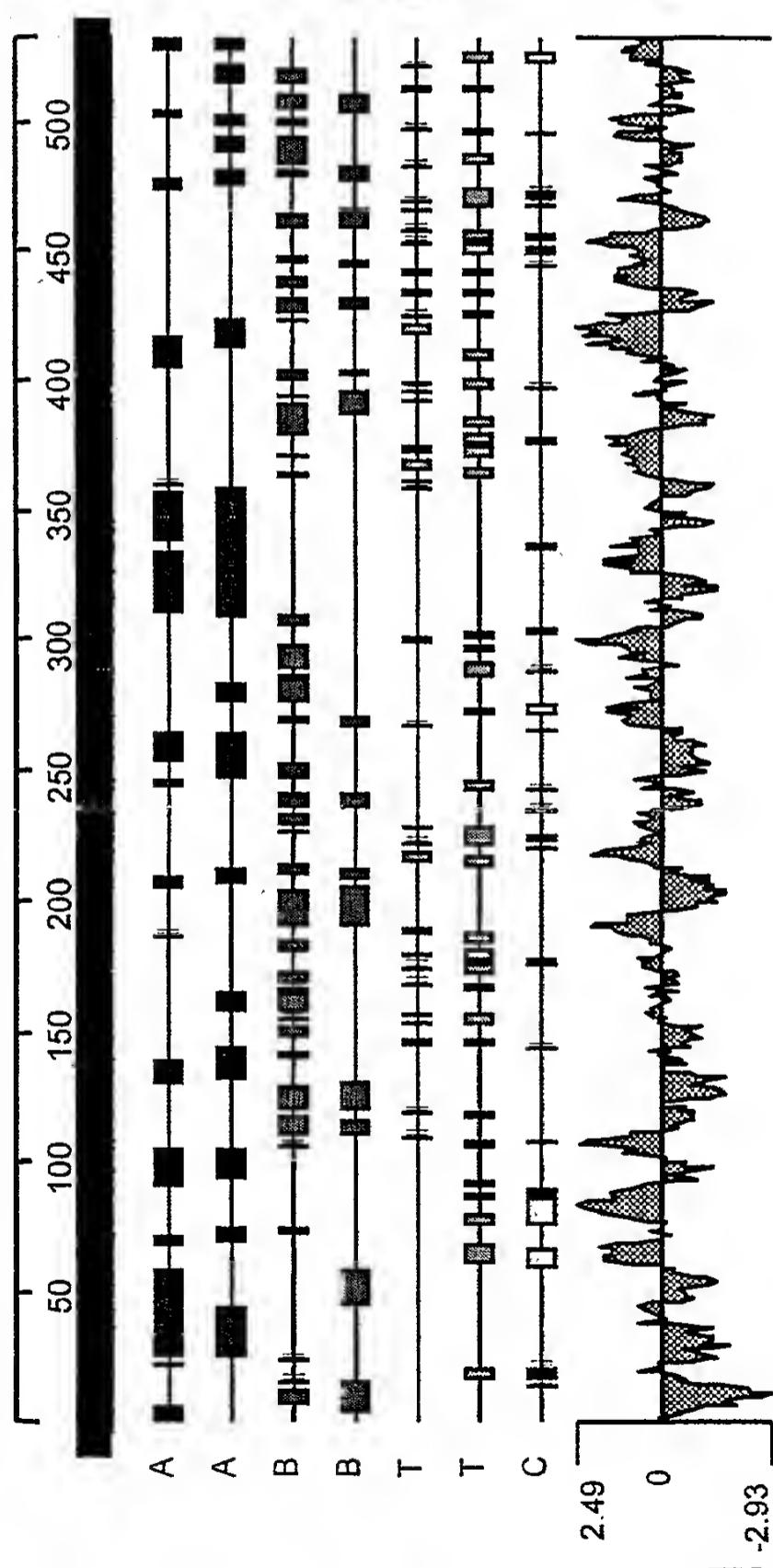
121 A S A R P P T S R R H V Y S G N L G P A F A G H S A G N I P D P V T S A Y A A S hPGRP-L aa Seq.
 530 ----- mPGRP-L aa Seq.

610

161 A Q P Q T Q P A C P F P S S hPGRP-L aa Seq.
 530 ----- N mPGRP-L aa Seq.

FIG. 3B





F/G. 5

